

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:40:12 : Search time 38.23 seconds  
(Without alignments)  
1100.523 Million cell updates/sec

Title: US-09-483-543a-8  
Perfect score: 1693  
Sequence: 1 KRCAGNDFSEERSWYGR.....QONPDEDFSGCGXGLEVLQ 318

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_16:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_unclassified:\*  
13: sp\_vertebrate:\*  
14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1078	63.7	239	11 Q9QW60	Q9QW60 mus sp. grb
2	834.5	49.3	255	14 Q9Q059	Q9Q059 avian sarco
3	343	20.3	279	5 Q9NHG3	Q9NHG3 caenorhabd
4	213	12.6	217	13 Q9PU11	Q9PU11 xenopus lae
5	200	11.8	600	5 Q9VE36	Q9VE36 drosophila
6	193	11.4	1067	13 Q9YH06	Q9YH06 xenopus lae
7	184.5	10.9	1010	13 Q9YH07	Q9YH07 xenopus lae
8	182	10.8	1097	5 Q9U2T9	Q9U2T9 caenorhabd
9	173	10.2	640	4 Q60593	Q60593 homo sapien
10	173	10.2	666	4 Q60592	Q60592 homo sapien
11	170	10.0	816	4 Q9UFT2	Q9UFT2 homo sapien
12	165	9.7	1270	13 Q42287	Q42287 xenopus lae
13	164	9.7	1196	11 Q35413	Q35413 rattus norv
14	163.5	9.7	857	3 Q9P7E8	Q9P7E8 schizosacch
15	163	9.6	684	4 Q9Y338	Q9Y338 homo sapien
16	162	9.6	815	4 Q9P200	Q9P200 homo sapien
17	162	9.6	1217	11 Q9WTE9	Q9WTE9 rattus norv
18	161	9.5	1094	5 Q61618	Q61618 drosophila
19	161	9.5	1097	5 Q9VIR7	Q9VIR7 drosophila

20	161	9.5	1100	4 Q94875	Q94875 homo sapien
21	160	9.5	1721	4 Q95216	Q95216 homo sapien
22	159	9.4	1220	4 Q9UET5	Q9UET5 homo sapien
23	159	9.4	1721	4 Q9UNK2	Q9UNK2 homo sapien
24	158	9.3	1004	4 Q9UHN7	Q9UHN7 homo sapien
25	158	9.3	1220	4 Q9UNK1	Q9UNK1 homo sapien
26	157.5	9.3	820	11 Q9Q2K2	Q9Q2K2 mus musculus
27	157	9.3	1248	4 Q9NZM2	Q9NZM2 homo sapien
28	157	9.3	1676	4 Q9ULG4	Q9ULG4 homo sapien
29	157	9.3	1681	4 Q9NYG0	Q9NYG0 homo sapien
30	157	9.3	1596	4 Q9NZM3	Q9NZM3 homo sapien
31	156.5	9.2	330	4 Q9NKB7	Q9NKB7 homo sapien
32	156.5	9.2	500	5 Q9V5J3	Q9V5J3 drosophila
33	156	9.2	509	5 Q24145	Q24145 drosophila
34	155	9.2	935	5 Q97337	Q97337 paracentrot
35	154.5	9.1	684	11 Q62417	Q62417 mus musculus
36	154.5	9.1	714	11 Q92028	Q92028 mus musculus
37	154.5	9.1	724	11 Q92029	Q92029 mus musculus
38	154	9.1	825	4 Q75815	Q75815 homo sapien
39	153	9.0	1714	11 Q920R4	Q920R4 mus musculus
40	152.5	9.0	1011	5 Q61639	Q61639 drosophila
41	152	9.0	954	5 Q97180	Q97180 drosophila
42	151.5	8.9	334	5 Q9RYT3	Q9RYT3 caenorhabd
43	151	8.9	1146	11 Q9WVE1	Q9WVE1 rattus norv
44	151	8.9	1186	5 Q61080	Q61080 acanthamoeb
45	150.5	8.9	687	11 Q9QY53	Q9QY53 mus musculus

## ALIGNMENTS

RESULT ID	1 Q9QW60	PRELIMINARY:	PRT:	239 AA.
AC	Q9QW60:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	GRB-3=EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN.			
OS	Mus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10095;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93028373; Pubmed=1409582;			
RA	Margolis B., Silvennoinen O., Comoglio F., Roonprapant C., Skolnik E.,			
RA	Ullrich A., Schlessinger J.,			
RT	High-efficiency expression/cloning of epidermal growth factor-			
RT	receptor-binding proteins with Src homology 2 domains.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).			
DR	HSSP: Q64010; 1CKA.			
DR	InterPro: IPR000980; -			
DR	InterPro: IPR001452; -			
DR	Pfam: PF00017; SH2; 1.			
DR	Pfam: PF00018; SH3; 1.			
DR	PRINTS: PR00401; SH2DOMAIN.			
DR	PRINTS: PR00452; SH3DOMAIN.			
DR	PROSITE: PS50001; SH2; 1.			
DR	PROSITE: PS50002; SH3; 1.			
DR	SMART: SM00326; SH3; 1.			
SO	SEQUENCE 239 AA; 26013 MW; 48326D680C9F09B6 CRC64;			

Query Match 63.7%; Score 1078; DB 11; Length 239;  
Best Local Similarity 99.5%; Pred. No. 8.6e-82;  
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	5	AGNDSEERSWYGRSLROEAVALLQGRHGVFLVDSSTSGDYLVLSYSENRSYSHYI 64
Db	33	AGNDSEERSWYGRSLROEAVALLQGRHGVFLVDSSTSGDYLVLSYSENRSYSHYI 92
Oy	65	INSSGPRPPVPPSPAPDPGVSPSLRLIGDPEFDSLALLEFYKIHVLDTTTLLIEPVANS 124

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Db 93 INSSGPRPPVPPSPAPGPPGVSPLRIGDQEDSLPALLEFKIHYLDTTTLEIEVANS 152
Qy 125 RQSGSVILROEAEYRALFDENGDEEDLPFKKGDLIRIRDRPEQWMAEDSEGRKG 184
Db 153 RQSGSVILROEAEYRALFDENGDEEDLPFKKGDLIRIRDRPEQWMAEDSEGRKG 212
Qy 185 IPVPYVEKRPASASVSALIGNOEGS 211
Db 213 IPVPYVEKRPASASVSALIGNOEGS 239

RESULT 2
Q99059 PRELIMINARY; PRT; 255 AA.
ID Q99059;
AC Q99059;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE GAG-CRK PROTEIN (FRAGMENT).
OS Avian sarcoma virus 1.
OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
OX NCBI_TaxID=11957;
RN [1]
RP MEDLINE=90045469; Pubmed=2554234;
RA Tsuchie H., Chang C.H.W., Yoshida M., Vogt P.K.;
RT "A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene."
RL Oncogene 4:1281-1284(1989).
CC -1 SIMILARITY: CONTAINS A COPY EACH OF THE SH2 AND SH3 DOMAINS.
DR EMBL: X17292; CA35181.1; -.
DR HSSP: O64010; ICKA.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR SMART: SM00326; SH3; 1.
KW Oncogene; Polyprotein; SH3 domain; SH2 domain.
FT NON_TER 1
FT DOMAIN 1 23 GAG (BY SIMILARITY).
FT DOMAIN 24 253 CRK (BY SIMILARITY).
FT DOMAIN 63 112 SH2 (OR B+C BOX) (BY SIMILARITY).
FT DOMAIN 188 239 SH3 (OR A BOX) (BY SIMILARITY).
FT DOMAIN 254 255 GAG (BY SIMILARITY).
SQ SEQUENCE 255 AA; 27985 MM; 0C562DOB2327A579 CRC64;

Query Match 49.3%; Score 834.5; DB 14; Length 255;
Best Local Similarity 78.3%; Pred. No. 1.5e-61;
Matches 159; Conservative 17; Mismatches 26; Indels 1; Gaps 1;
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RESULT 3
Q9NHC3 PRELIMINARY; PRT; 279 AA.
ID Q9NHC3;
AC Q9NHC3;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE CELL-CORPSE ENGULFMENT PROTEIN CED-2.
GN CED-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Reddien P.W., Horvitz H.R.;
RT "CED-2/CrklI and CED-10/Rac control phagocytosis and cell migration in C. elegans."
RL Nat. Cell Biol. 0:0-0(2000).
DR EMBL: AF226866; AAF33845.1; -.
DR InterPro: IPR000980; -.
DR InterPro: IPR001452; -.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 2.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
SQ SEQUENCE 279 AA; 30878 MM; 5CE7DA478948970B CRC64;
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Query Match 20.3%; Score 343; DB 5; Length 279;
Best Local Similarity 31.0%; Pred. No. 9.9e-21;
Matches 93; Conservative 52; Mismatches 111; Indels 44; Gaps 9;

Qy 8 FDSEBRSSWYGRSLROEAVALLQGRH--GVLVNDSTSPGDYLVY--SENSRVS 61
Db 6 FDPFMRSEFYFGMSREBAHRL-GEPOVSIGTFLMDDS-RPEVSLVREADEGNAVC 63
Qy 62 HYIINSGPRPPVPPSPAPGPPGVSPLRIGDQEDSLPALLEFKIHYLDTTTLEIEV 121
Db 64 HYLIERGEPRK-----EDGTAAGVKTANOSFPDIPALNHFMKRVLTASL-- 110
Qy 122 ASRQSGSVILROEAEYRALFDENGDEEDLPFKKGDLIRIRDRPEQWMAEDSEGRK 181
Db 111 -----AAKKKPILEVVGTFPFNGERTDLPFEGGERLEILSKTNQDWEARNALGT 162
Qy 182 RGMIVPPVVE--KYRPASASVSALIGNOEGSHPQPLGCPPEGPYAPQSVNTPPLRLQ 237
Db 163 TGLVPAANTVOIOMEFHNDRTS-----KGASQSSIGSGGGAERFSSASTSSDIEL 213
Qy 238 --NGPIYAVRIQKRPVNAVDKTALEVEGLVTKINVSQWEGECNGRGHPFTHYR 295
Db 214 QPRLPAKAKVTFDRKPAIYDPTQLRVKKGGQVLYVTQKMSNOMYAEILDGIGSPHYLR 273

RESULT 4
Q9PU11 PRELIMINARY; PRT; 217 AA.
ID Q9PU11;
AC Q9PU11;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE GRB2 PROTEIN.
GN GRB2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RA Golaset C., Shi D.L., Boucaut J.C.;
```

"Selective inhibition of neural induction but not mesoderm induction by interfering mutants of *sem-5/grd-2*." RT  
 RI Submitted (DDB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF123061: CABS9279.1; -.  
 DR HSP: P29354; 1GHTU.  
 DR InterPro: IPR00108; -.  
 DR InterPro: IPR000980; -.  
 DR InterPro: IPR001452; -.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH2; 2.  
 DR PRINTS: PR00499; P67PHOX.  
 DR PRINTS: PR00401; SH2DOWN.  
 DR PRINTS: PR00452; SH2DOWN.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 2.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00326; SH3; 2.  
 SO SEQUENCE 217 AA; 25135 MW; 2349A8260F9D4CD CRC64;

Query Match 12.6%; Score 213; DB 13; Length 217;  
 Best Local Similarity 27.4%; Pred. No. 4.3e-10;  
 Matches 52; Conservative 45; Mismatches 57; Indels 36; Gaps 7;

QY 7 NPDSESSWTWGRSLRQEAVALIQQGRH-GVFLVRDSSISPDYVLSVSENSRYSHYIT 65  
 Db 51 NYIEKKAHPWFFGKIPRAKAEEMIGKORHDAFLIRESEAPGDFSLSVKFGNDVQHFKV 110  
 QY 66 NSSGRRPPVPPSPAPPGVSPSRIRIGDQEDFSLPALLEYKIHLYDTTLIPVRSR 125  
 Db 111 LRDG-----AGKFLWVVFNSLNLVYDHR-----STIS---VSRNQ 144  
 QY 126 QSGGVILRQ-----EAEYVRLDFDNGNDEDLPEFKGDIIRIRDKPEQWMAEDSEG 180  
 Db 145 Q---TFLMDIQVPPQPIYQALFDGDFDQEDGELGFRGDFLTQYVNDSPWMMWG-TCLIS 200  
 QY 181 KRGMIPVRYV 190  
 Db 201 QTGMFPRMYV 210

RESULT 5  
 QY9E96 PRELIMINARY; PRT; 600 AA.  
 AC QY9E96;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE CG7129 PROTEIN.  
 GN CG7129.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R., Champe M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cackley E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harlos N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon S., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wattarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003721; AAP5531.1; -.  
 DR HSP: P29354; 1GFC.  
 DR FlyBase: FBgn0038599; CG7129.  
 DR InterPro: IPR00108; -.  
 DR InterPro: IPR001452; -.  
 DR Pfam: PF00018; SH3; 2.  
 DR PRINTS: PR00499; P67PHOX.  
 DR PRINTS: PR00452; SH2DOWN.  
 DR PROSITE: PS50002; SH3; 2.  
 DR SMART: SM00326; SH3; 1.  
 SO SEQUENCE 600 AA; 62961 MW; 9E3BA36C4A165A3 CRC64;

Query Match 11.8%; Score 200; DB 5; Length 600;  
 Best Local Similarity 25.4%; Pred. No. 2e-08;  
 Matches 63; Conservative 35; Mismatches 90; Indels 60; Gaps 8;

QY 61 SHYIINSSGRRPPVPPSPAPPGVSPSRIRIGDQEDFSLPALLEYKIHLYDTTLIP 120  
 Db 396 SGVAGSTPPSPWPKGPPPPPPASSGGSISLDVINGKDAL-----A 439  
 QY 121 VARSQSGVILRQEAVALIQQGRH-GVFLVRDSSISPDYVLSVSENSRYSHYIT 180  
 Db 440 LSNCCG---YMEEEVYPAVALYDFGDIPEGDLSPREGEKTYLLDHPPEWLRGRTSG 496  
 QY 181 KRGMIPVRYVKKYPASVYALIGNQESHPQPLGPEPGYAPSVNTPLPNLQNGP 240  
 Db 497 CEGIFPINYVDIKVPLGAT-----GGAAMAFASMAAPSPSS----- 534  
 QY 241 IYAVIQRVPMX-----DKTALALEVGLVYKTKINVSQW-EGSCNKRGRHPP 291  
 Db 535 -----QQQLPTALCLYHPGEVEGDLAQENELVTL-YRINEDMLYGEVAGRGQFP 586  
 QY 292 THVRLDQ 299  
 Db 587 --ANFLDQ 592

RESULT 6  
 QY9H06 PRELIMINARY; PRT; 1067 AA.  
 AC QY9H06;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE PHOSPHOLIPASE C-GAMMA-1B (FRAGMENT).  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; *Xenopus*.



QY 122 ARSOGSGVILROEAEY-----VRAFDENGDEEDLPFKKGLIRIRDKP 168  
 Db 558 GTPDDPGALYEGRNPGFYEAAMPPTFKCSYALPFDYAOERDELFTFKNTILIQVEKO 617  
 QY 169 EECMMNAEDSEGRGM-IPYVYEK-YRPASASVALLIGNOEGSHIPOLGPEPGPIA 226  
 Db 618 EGGWNRG-DCGGKKOMFPANMEITSP-----PEPPERQ 653

QY 227 P-SVNPPLPNLON 239  
 Db 654 HLDENSPLGLDG 667

RESULT 8  
 Q902T9 PRELIMINARY; PRT; 1097 AA.  
 AC Q902T9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Y116A8C.36 PROTEIN.  
 GN Y116A8C.36.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peleiderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurtry A.A.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9069613; PubMed=9851916;  
 RA none;  
 RT "genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology";  
 RL Science 282:2012-2018(1998).  
 CC -1- SIMILARITY: TO EF-HAND FAMILY.  
 DR EMBL: AL117204; CAB55138.1; -.  
 DR HSSP: P29355; ISEM.  
 DR InterPro: IPR00108; -.  
 DR InterPro: IPR00194; -.  
 DR InterPro: IPR000261; -.  
 DR InterPro: IPR001452; -.  
 DR InterPro: IPR002048; -.  
 DR Pfam: PF00018; SH3; 5.  
 DR Pfam: PF00036; ehand; 2.  
 DR PRINTS: PR00499; P67PHOX.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PROSITE: PS00152; ATPASE ALPHA, BETA; UNKNOWN\_1.  
 DR PROSITE: PS00018; EF\_HAND; UNKNOWN\_2.  
 DR PROSITE: PS50002; SH3; 5.  
 DR SMART: SM00054; EFH; 1.  
 KW Calcium-binding.  
 SQ SEQUENCE 1097 AA; 122071 MW; 1C2BA5F103968372 CRC64;

Query Match 10.8%; Score 182; DB 5; Length 1097;  
 Best Local Similarity 21.2%; Pred. No. 1.4e-06;  
 Matches 75; Conservative 56; Mismatches 144; Indels 78; Gaps 14;

QY 6 GNFDSERSSWY--WGRLSROEAVA-LLOGQRH-----GVFLVRDS----- 43  
 Db 627 GEFKDTASGRFDADFGATSTADPAQIAQAPAHSGAVDQSAFNHIDYKCRALFAFEA 686  
 QY 44 -STSGDDYLVASENS-----RVSHY-----INSSGPRPPVP 76  
 Db 687 RSEDELSEFEDVITIVQSHAEFGWAGOLREKVGWFPFAVEAIAAVPTREGDPION 746  
 QY 77 SPAOPPGVSPSLRIGDOEFDSLPALEFYKTHVDTTLLIEPVARSOGSGVILROE 136  
 Db 747 MPMMTFSSSVSDOIGVAKRAKAEIAA-----MGITFGAPASSAPAAAVATISQCI 798

QY 137 AEYVRALEDNGNDEEDLPFKKGLIRIRDKPEQOMNAEDSEGRGMIPYVYEKYPRA 196  
 Db 799 AQ-----FQRRANNEEDLSPAKGDTIEVLEK-QEMMKGRNPAGEIGMPSKYVEVAT 852  
 QY 197 SASVSALIGNOEGSHIPOLGPEPGPIAOPSY--NTPPLMLONCP---IYARIQKRV 250  
 Db 853 TSTTPPIVSPSKASA-----GAPGAAGAQYDVPSDVLQSETPAFOOQLYTVIYDF- 905  
 QY 251 PNAYDKTALAEVGLVYKIVNSGOWEGEGCKRGHPFPHVRLLOQOND 303  
 Db 906 -EAVETTDALHVGDTILVEKN-DEMMKGRNGRGIRIPANVVEISVQAGD 956

RESULT 9  
 ID 060593 PRELIMINARY; PRT; 640 AA.  
 AC 060593;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE ARG/ABL-INTERACTING PROTEIN ARGBP2B (FRAGMENT).  
 GN ARGBP2B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97362243; PubMed=9211900;  
 RA Wang B., Golemis E.A., Krush G.D.;  
 RT "ArgBP2, a multiple Src homology 3 domain-containing, Arg/ABL-  
 RT interacting protein, is phosphorylated in v-Abl-transformed cells and  
 RT localized in stress fibers and cardiocyte Z-disks.";  
 RL J. Biol. Chem. 272:17542-17550(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wang B., Golemis E.A., Krush G.D.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF049685; AAC05509.1; -.  
 DR HSSP: P29354; IGR1.  
 DR InterPro: IPR00108; -.  
 DR InterPro: IPR001452; -.  
 DR InterPro: IPR002965; -.  
 DR InterPro: IPR003127; -.  
 DR Pfam: PF00018; SH3; 2.  
 DR Pfam: PF02208; Sorb; 1.  
 DR PRINTS: PR00499; P67PHOX.  
 DR PRINTS: PR01217; PRICHTEXTENS.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PROSITE: PS50002; SH3; 2.  
 DR SMART: SM00326; SH3; 1.  
 FT NON\_TER 640 640  
 SQ SEQUENCE 640 AA; 70660 MW; 030A8C5036331674 CRC64;

Query Match 10.2%; Score 173; DB 4; Length 640;  
 Best Local Similarity 26.0%; Pred. No. 3.7e-06;  
 Matches 72; Conservative 29; Mismatches 92; Indels 84; Gaps 12;

QY 43 SSISPGDYIVSVSENSVSHYIINSSGPRPPVPPSAQPP-----PGVSPRLRIG 93  
 Db 393 SRTSPGVDLPJGSSYTLTKSP--TSSSPSPSRVAKDRESRYSSTLDMGSAFRERRG 450  
 QY 94 DQFEDSLPALLEFYKTHVDTTLLIEPVARSOGSGVILROEAEYVRLPFGNDEED 153  
 Db 451 TPKEKELPA-----KAVYEFKAQTSKE 472  
 QY 154 LPFKKGLIRIRDKPEQOMNAEDSEGRGMIPYVYEKYPASASVALLIGNOEGSH 213  
 Db 473 LSFKKGDTVILRKIDNMGEG-HHGRVGIFPISYVEKLT----- 513  
 QY 214 QPLGPPPGYAPQPSVNTPLPNLONGPYARVYOKRVPAVYDKTALAEVGLVYKTKIN 273



Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO EF-HAND FAMILY.  
 DR EMBL: AF032118; AAC73068.1; -.  
 DR HSSP: P29355; ISEM  
 DR InterPro: IPR000261; -.  
 DR InterPro: IPR001452; -.  
 DR InterPro: IPR002048; -.  
 DR Pfam: PF00018; SH3; 5.  
 DR Pfam: PF00036; ehand; 2.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PROSITE: PS00018; EF\_HAND; UNKNOWN\_2.  
 DR PROSITE: PS50002; SH3; 5.  
 DR SMART: SM00027; EH; 1.  
 DR Calcium-binding.  
 SO SEQUENCE 1270 AA; 143670 MW; EA940C1F6B6A6858 CRC64;

Query Match 9.7%; Score 165; DB 13; Length 1270;  
 Best Local Similarity 24.5%; Pred. No. 4.3e-05;  
 Matches 75; Conservative 38; Mismatches 79; Indels 114; Gaps 18;

QY 11 EERSWVGRSLRQEAVALLOGRHGVFLVADSSSPGDIYLSVSENSRSHYLIINSGP 70  
 DB 928 EQQDMWVFG-----VQGQK-GWF-----PKSYKILSGPLKSTSIDSTSE 969  
 QY 71 RPPVPPSPAPPPGVSPSRIRIGDQFDSLPALEFYKIHLYDTTTLIEPARSRQSGV 130  
 DB 970 SP-----ASLKRVSAPFK-PAI-----QGF-- 989  
 QY 131 ILROEAAYRALDFENGDEEDLPFKKGDIILIRDKPEEQMNAEDSEGRKMIIPVYV 190  
 DB 990 -----YXI-SMYYESNEGDILFQGGDLI-VVKKKGDMWGTGVE-KTGVFSPMYV 1039  
 QY 191 EKYRPASVSVALIGNQSGHPQLGPEPGPYAQSVPNTPLPLAQSPYARIQKRV 250  
 DB 1040 ---RPKDSEAG--SGGTGS-----LGKKPLAQYIA--- 1067  
 QY 251 PNAYDKTA---LALFVGLVYVTKLVNSGQEGE--CNGKR---GHFPTVHRL---D 298  
 DB 1068 --SVATAPEQDITLAPGQILIRKKNPGWEGELQANGKKRQJGWFPANYVKLLSPGTN 1125  
 QY 299 QONPDE 304  
 DB 1126 KSTPTE 1131

RESULT 13  
 ID 035413 PRELIMINARY; PRT; 1196 AA.  
 AC 035413;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE SH3-CONTAINING PROTEIN P4015.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ide N., Takeuchi M., Hata Y., Takai Y.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF026505; AAB81527.1; -.  
 DR HSSP: P29354; IGR1.  
 DR InterPro: IPR000822; -.  
 DR InterPro: IPR001452; -.  
 DR InterPro: IPR003127; -.  
 DR Pfam: PF00018; SH3; 3.  
 DR Pfam: PF02208; Sorb; 1.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR ProDom: PD016158; -; 1.  
 DR PROSITE: PS50002; SH3; 3.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2; UNKNOWN\_1.

DR SMART: SM00326; SH3; 1.  
 SO SEQUENCE 1196 AA; 134052 MW; 84EB1DFD604D4884 CRC64;

Query Match 9.7%; Score 164; DB 11; Length 1196;  
 Best Local Similarity 29.1%; Pred. No. 4.8e-05;  
 Matches 57; Conservative 31; Mismatches 70; Indels 38; Gaps 10;

QY 115 TTLIEPARSRQSGVYLIRQEAAYRALDFENGDEEDLPFKKGDIILIRDKPEEQMNA 174  
 DB 942 TDGGRSVSRERRGTP---EEVVKLPAAKAYDFKAQTSKELSFKGGDTYILRKIDQNWYE 998  
 QY 175 AEDSEGRKMIIPVYVEKTRPASASVALIGNQSGHPQLGPEPGPYAQSVPNTPLP 234  
 DB 999 GE-HHGRVGIPIPSYVEKLP-----PEK--AQPA--RPP 1029  
 QY 235 NLONGPIYARVIOKRVPNADKTALEVEGLVYTKINVSQGW-EGECNG--KRGHPF 291  
 DB 1030 PVQGGEL-GEALIKYFNENALTNVELSLRKGDRILLIK-RYDQWNYGKTIPTNRQGIPTV 1087  
 QY 292 THVRLDQNP-DEDF 306  
 DB 1088 SYVEVYKRNTRKSGEDY 1103

RESULT 14  
 ID 09P7E8 PRELIMINARY; PRT; 857 AA.  
 AC 09P7E8;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE ACTIN BINDING PROTEIN WITH SH3 DOMAINS.  
 GN SPADJ60.02C.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_Taxid=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Harris D., Wood V., Rajandream M.A., Barrell B.G.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL162631; CAB83085.1; -.  
 DR InterPro: IPR000108; -.  
 DR InterPro: IPR001452; -.  
 DR InterPro: IPR002108; -.  
 DR InterPro: IPR002965; -.  
 DR Pfam: PF00018; SH3; 2.  
 DR Pfam: PF00241; cofilin\_ADF; 1.  
 DR PRINTS: PR00499; P67PHOX.  
 DR PRINTS: PR01217; PRICHEXTENSN.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PROSITE: PS50002; SH3; 2.  
 DR SMART: SM00102; ADF; 1.  
 SO SEQUENCE 857 AA; 91137 MW; 247EFA78BAE7097 CRC64;

Query Match 9.7%; Score 163.5; DB 3; Length 857;  
 Best Local Similarity 23.8%; Pred. No. 3.4e-05;  
 Matches 57; Conservative 35; Mismatches 87; Indels 61; Gaps 9;

QY 68 SGRRP-----VPPSPAPPPGVSPSRIRIGDQFDSLPALEFYKIHLYDTTTLIEPVAR 123  
 DB 663 SVQPPAPAPVPEVPSVQPPAVYVEAGQLNPPVPLPBP-----DETQ--EP--- 711  
 QY 124 SRQSGVYLIRQEAAYR---ALFDENGDEEDLPFKKGDIILIRDKPEEQMNAEDSE 179  
 DB 712 --QVGDVKATEHQPTKTPAIVYIDYSPEDENIELVENQDILIEFVDGGMVLGNSK 769  
 QY 180 GKRGMIPVYVEKTRPASASVALIGNQSGHPQLGPEPGPYAQSVPNTPLPLNLQNG 239

Db 770 GQCGLFPSNVE-----ITGPNETANNP-----AEPQAGP----- 801  
QY 240 PIYARVIOKRVNAYDKTA-----LALVEGELVKTKINVGWEGECNGKRCHFPPTHV 294  
Db 802 -----GKSVKAIYDVAQAEDEDELIFANVDCVDPNMWEGEGCHGRGLFPSNVY 854  
RESULT 15  
QY338  
ID QY338 PRELIMINARY; PRT; 684 AA.  
AC QY338;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE SH3P12 PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Lin W.S., Chuang L.M.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF136380; AAD27647.1; -.  
DR HSSP: Q60631; IGBO.  
DR InterPro: IPR00108; -.  
DR InterPro: IPR001452; -.  
DR InterPro: IPR003127; -.  
DR Pfam: PF00018; SH3; 3.  
DR Pfam: PF02208; Sorb; 1.  
DR PRINTS: PR00499; P67PHOX.  
DR PRINTS: PR00452; SH3DOMAIN.  
DR PROSITE: PSS0002; SH3; 3.  
DR SMART: SM00326; SH3; 1.  
SQ SEQUENCE 684 AA; 76341 MW; 2274E632BB07329C CRC64;

Query Match 9 6%; Score 163; DB 4; Length 684;  
Best Local Similarity 25.0%; Pred. NO. 2.8e-05;  
Matches 67; Conservative 40; Mismatches 103; Indels 58; Gaps 12;

QY 41 RDSSTSPGDVYLSVSENSRYSHYTIINSSGPRPPVPPSPAQPPGVSPSLRLIGDQEFDSL 100  
Db 369 RESDCAFGD--LTSLENSQIYKSVLEGVTPIQDLSGLKRPSSASTKNSESPRLF--I 424  
QY 101 PALLEFKIHLDTTTLIEPVARSQSGVILKQEEAFYRALFDENGDEEDLPFKKGD 160  
Db 425 PA-----DYLEST---EEFIRRRHD-----DKEMRPARAKFDPKAQTTLKELPLQKGD 468  
QY 161 ILIRDRPEEQWMAEDESEGRGMIPVYEKYPASASVSALIGNQEGSHPOPLGPE 220  
Db 469 IVYIKQIDQWVYEGE-IHSGVGIFFRTYIELLPAAK----- 505  
QY 221 PGYPAQDSVNTPLPNLQNGPIYARVIOKRVNAYDKTALALEVGEVLYKTKINVGW--E 279  
Db 506 ----AQPKKLTTPQVYLE----YGEAIAKFNFNNGDTQVEMSFRRGERITLLR--QVDENWYE 556  
QY 280 GECNG--KRGHPFTTHVRLDQ---QNP 302  
Db 557 GRIPGTSRQGIFFITYVDVIKRLPLVKNP 584

Search completed: September 27, 2001, 16:43:09  
Job time: 177 sec